

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	33396	XU.INV.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:05
L2	10469	\$atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:05
L3	35397	digoxin or digitoxin or ouabain OR GLYCOSIDE\$2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:06
L5	11	1 AND 2 AND 3	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:07
L6	336356	(ANTIBOD\$3 OR IMMUNOGLOBULIN\$4 OR IMMUN\$2GLOBULIN\$4 OR GAMMA\$1GLOBULIN\$4 OR MAB\$10 OR Fab\$1 OR fab\$4sub\$10 OR hybridoma\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:14
L7	1283	2 AND 3 AND 6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:14
L8	1319	anti-na\$12 OR anti-NKA	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:15
L9	20	7 AND 8	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2007/05/08 16:15

(FILE 'HOME' ENTERED AT 16:16:41 ON 08 MAY 2007)

FILE 'MEDLINE, CAPLUS, EMBASE, BIOSIS' ENTERED AT 16:17:21 ON 08 MAY 2007

L1	117 S XU/AU
L2	1 S RSATEEEPPNDD
L3	0 S L1 AND L2
L4	72922 S INOTROP?
L5	0 S L4 AND L1
L6	5224 S XU K?/AU
L7	38 S L6 AND L4

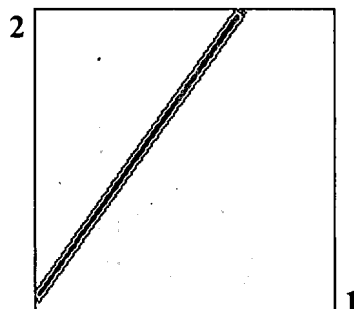
## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter: ☐ View option:   
 Masking character option:  Masking color option:   
☐ Show CDS translation

Sequence 1: lcl|AAA416701\_Rat\_NaK  
Length = 1023 (1 .. 1023)

Sequence 2: lcl|SEQ\_ID\_NO:745  
Length = 750 (1 .. 750)

*Rosen et al.*



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1381 bits (3575), Expect = 0.0, Method: Composition-based stats.  
Identities = 673/712 (94%), Positives = 689/712 (96%), Gaps = 5/712 (0%)

Query	1	MGKGVGRDKYEPAAVSEHGDKKSKKAKKERDMDDELKKEVSMDDHKLSLDELHRKYGTDLS	60
		MGKGVGRDKYEPAAVSE GDKK KK KK+RMDDELKKEVSMDDHKLSLDELHRKYGTDLS	
Sbjct	37	MGKGVGRDKYEPAAVSEQGDKKGGKGGKDRDMDDELKKEVSMDDHKLSLDELHRKYGTDLS	96
Query	61	RGLTPARPVEILARDGPNALTTPPTTPEWVKFCRQLFGGFSMLLWIGAILCFLAYGIRSA	120
		RGLT AR EILARDGPNALTTPPTTPEW+KFCRQLFGGFSMLLWIGAILCFLAY I++A	
Sbjct	97	RGLTSARAAEILARDGPNALTTPPTTPEWIKFCRQLFGGFSMLLWIGAILCFLAYSIOAA	156
Query	121	TEEEPPNDLLYLGVVLSAVVIITGCFSYQEAQSSKIMESFKNMVPQQALVIRNEEKMSI	180
		TEEEP. ND+LYLGVVLSAVVIITGCFSYQEAQSSKIMESFKNMVPQQALVIRN EKMSI	
Sbjct	157	TEEEPQNDNLYLGVVLSAVVIITGCFSYQEAQSSKIMESFKNMVPQQALVIRNGEKMSI	216
Query	181	NAEDVVVVDLVEVKGGDRIPADLRISANGCKVDNSSLTGESEPQTRSPDFTNENPLETR	240
		NAE+VVV DLVEVKGGDRIPADLRISANGCKVDNSSLTGESEPQTRSPDFTNENPLETR	
Sbjct	217	NAEEVVVGDLVEVKGGDRIPADLRISANGCKVDNSSLTGESEPQTRSPDFTNENPLETR	276
Query	241	NIAFFSTNCVEGTARGIVVYTGDRITVMGRIATLASGLEGGQTPIAEEIEHFIHLITGVAV	300
		NIAFFSTNCVEGTARGIVVYTGDRITVMGRIATLASGLEGGQTPIA EIEHFIH+ITGVAV	
Sbjct	277	NIAFFSTNCVEGTARGIVVYTGDRITVMGRIATLASGLEGGQTPIAEEIEHFIHIITGVAV	336
Query	301	FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEVLLATVTVCLTLTAKRMARKNCLVKN	360

Sbjct	337	FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPE LLATVTVCLTLTAKRMARKNCLVKN	396
Query	361	LEAVETLGSTSTICSDKTGTLTQNRMTVAHMFWDNQIHEADTTENQSGVSFDKTSATWFA	420
Sbjct	397	LEAVETLGSTSTICSDKTGTLTQNRMTVAHMFWDNQIHEADTTENQSGVSFDKTSATW A	456
Query	421	LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIEVCCGSVMEMREKYTKIVEI	480
Sbjct	457	LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIE+CCGSV EMRE+Y KIVEI	516
Query	481	PFNSTNKYQLSIHKNPNASEPKHLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN	540
Sbjct	517	PFNSTNKYQLSIHKNPNTSEPQHLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN	576
Query	541	AYLELGGLGERVLGFCHLLLPDEQFPEGFQFDTDEVNFPVDNLCFVGLISMIDPPRAAVP	600
Sbjct	577	AYLELGGLGERVLGFCHL LPDEQFPEGFQFDTD+VNFP+DNLCFVGLISMIDPPRAAVP	636
Query	601	DAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAARLNIPVNQVNPRDA	660
Sbjct	637	DAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAARLNIPV+QVNPRDA	696
Query	661	KACVVHGSDLKDMTSEELDDILRYHTEIVFARTSPQQKLIIVE-----GCQR	707
Sbjct	697	KACVVHGSDLKDMTSE+LDDIL+YHTEIVFA+TSPQQKLIIVE GC R	748

CPU time:        0.03 user secs.            0.01 sys. secs            0.04 total secs.



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

4 pages of  
aligned  
seqs.

28  
5-7-07

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

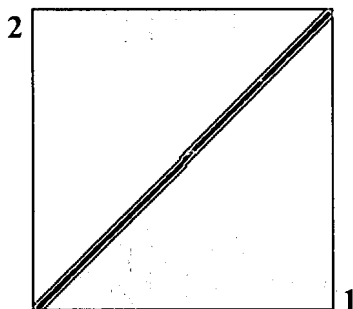
Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **0** expect: **10.000** wordsize: **3** Filter ☐ View option **Standard**  
Masking character option **X for protein, n for nucleotide** Masking color option **Black**  
☐ Show CDS translation **Align**

Sequence 1: lcl|rat\_NaK  
Length = 1023 (1 .. 1023)

Genbank Acc # AAA41671

Sequence 2: lcl|human\_NaK  
Length = 1023 (1 .. 1023)

Genbank Acc # NP\_000692



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 2051 bits (5315), Expect = 0.0, Method: Composition-based stats.  
Identities = 985/1023 (96%), Positives = 1001/1023 (97%), Gaps = 0/1023 (0%)

Query	1	MGKGVGRDKYEPAAVSEHGDKKSKKAKKERDMDLKKKEVSMDDHKLSLDELHRKYGTDLS	60
		MGKGVGRDKYEPAAVSE GDKK KK KK+RDMDELKKKEVSMDDHKLSLDELHRKYGTDLS	
Sbjct	1	MGKGVGRDKYEPAAVSEQGDKKGKKGKDRDMDLKKKEVSMDDHKLSLDELHRKYGTDLS	60
Query	61	RGLTPARPVEILARDGPNALTTPPTTPEWVKFCRQLFGGFSMLLWIGAILCFLAYGIRSA	120
		RGLT AR EILARDGPNALTTPPTTPEW+KFCRQLFGGFSMLLWIGAILCFLAY I++A	
Sbjct	61	RGLTSARAAEILARDGPNALTTPPTTPEWIKFCRQLFGGFSMLLWIGAILCFLAYSIDAA	120
Query	121	TEEEPPNDDL LYLGVVLSAVVIITGCFSYYQEAQSSKIMESFKNMVPPQALVIRNEEKMSI	180
		TEEEP ND+LYLGVVLSAVVIITGCFSYYQEAQSSKIMESFKNMVPPQALVIRN EKMSI	
Sbjct	121	TEEEPQNDNL LYLGVVLSAVVIITGCFSYYQEAQSSKIMESFKNMVPPQALVIRNGEKMSI	180
Query	181	NAEDVVVVDLVEVKGGDRIPADLRIISANGCKVDNSSLTGESEPPQTRSPDFTNENPLETR	240
		NAE+VVV DLVEVKGGDRIPADLRIISANGCKVDNSSLTGESEPPQTRSPDFTNENPLETR	
Sbjct	181	NAEEVVVGDLVEVKGGDRIPADLRIISANGCKVDNSSLTGESEPPQTRSPDFTNENPLETR	240
Query	241	NIAFFSTNCVEGTARGIVVYTGDRVTMGRIATLASGLEGGQTPIAEEIEHFIHLITGVAV	300
		NIAFFSTNCVEGTARGIVVYTGDRVTMGRIATLASGLEGGQTPIA EIEHFIH+ITGVAV	
Sbjct	241	NIAFFSTNCVEGTARGIVVYTGDRVTMGRIATLASGLEGGQTPIAABIEHFIHIITGVAV	300
Query	301	FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEVLLATVTVCLTLTAKRMARKNCLVKN	360

Sbjct	301	FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPE LLATVTVCLTLTAKRMARKNCLVKN FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKN	360
Query	361	LEAVETLGSTSTICSDBKTGTLTQNRMTVAHMMWFDNQIHEADTTENQSGVSFDKTSATWFA LEAVETLGSTSTICSDBKTGTLTQNRMTVAHMMWFDNQIHEADTTENQSGVSFDKTSATW A	420
Sbjct	361	LEAVETLGSTSTICSDBKTGTLTQNRMTVAHMMWFDNQIHEADTTENQSGVSFDKTSATWLA	420
Query	421	LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIEVCCGSVMEMREKYTKIVEI LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIE+CCGSV EMRE+Y KIVEI	480
Sbjct	421	LSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIELCCGSVKEMRERYAKIVEI	480
Query	481	PFNSTNKYQLSIHKPNPASEPKHLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN PFNSTNKYQLSIHKPNP SEP+HLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN	540
Sbjct	481	PFNSTNKYQLSIHKPNPTSEPQHLLVMKGAPERILDRCSSILLHGKEQPLDEELKDAFQN	540
Query	541	AYLELGGGLGERVLGFCHLLLPDEQFPEGFQFDTDEVNFPVDNLCFVGLISMIDPPRAAVP AYLELGGGLGERVLGFCHL LPDEQFPEGFQFDTD+VNFP+DNLCFVGLISMIDPPRAAVP	600
Sbjct	541	AYLELGGGLGERVLGFCHLFLPDEQFPEGFQFDTDDVNFPIDNLCFVGLISMIDPPRAAVP	600
Query	601	DAVGKCRSAGIKVIMVTGDHPITAKAIAGVGIIISEGNETVEDIAARLNIPVNQVNPRDA DAVGKCRSAGIKVIMVTGDHPITAKAIAGVGIIISEGNETVEDIAARLNIPV+QVNPRDA	660
Sbjct	601	DAVGKCRSAGIKVIMVTGDHPITAKAIAGVGIIISEGNETVEDIAARLNIPVSQVNPRDA	660
Query	661	KACVVHGSDDLKDMTSEELDDILRYHTEIVFARTSPQQKLIIVEGCQRQGAIVAVTGDGVN KACVVHGSDDLKDMTSE+LDDIL+YHTEIVFARTSPQQKLIIVEGCQRQGAIVAVTGDGVN	720
Sbjct	661	KACVVHGSDDLKDMTSEQLDDILKYHTEIVFARTSPQQKLIIVEGCQRQGAIVAVTGDGVN	720
Query	721	DSPALKKADIGVAMGIVGSDVSKQAADMILLDDNFASIVTGVEEGRILFDNLKKSIAAYTL DSPALKKADIGVAMGI GSDVSKQAADMILLDDNFASIVTGVEEGRILFDNLKKSIAAYTL	780
Sbjct	721	DSPALKKADIGVAMGIAGSDVSKQAADMILLDDNFASIVTGVEEGRILFDNLKKSIAAYTL	780
Query	781	TSNIPEITPFLIFIIANIPLPLGTVTILCIDLGTMVPAISLAYEQAESDIMKRQPRNPK TSNIPEITPFLIFIIANIPLPLGTVTILCIDLGTMVPAISLAYEQAESDIMKRQPRNPK	840
Sbjct	781	TSNIPEITPFLIFIIANIPLPLGTVTILCIDLGTMVPAISLAYEQAESDIMKRQPRNPK	840
Query	841	TDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLPFHLLGIRETWDDRWINDEV TDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLP HLLG+R WDDRWINDEV	900
Sbjct	841	TDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLPIHLLGLRVDWDDRWINDEV	900
Query	901	SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFE SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFE	960
Sbjct	901	SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFE	960
Query	961	ETALAFLSYCPMGGAALRMYPLKPTWWFCAFPYSLLIFVYDEVKLIIRRRPGGWVEKE ETALAFLSYCPMG ALRMYPLKPTWWFCAFPYSLLIFVYDEVKLIIRRRPGGWVEKE	1020
Sbjct	961	ETALAFLSYCPMGVALRMYPLKPTWWFCAFPYSLLIFVYDEVKLIIRRRPGGWVEKE	1020
Query	1021	TTY 1023 TTY	
Sbjct	1021	TTY 1023	

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.